

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 19:52:11 ; Search time 49.48 Seconds

(without alignments)
219.297 Million cell updates/sec

Title: US-09-481-990-2

Perfect score: 1753

Sequence: 1 MQLSLAGSSCVRLVERHRSR.....QNE?FVATQSSACVDPANH 336

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SWISSPROT_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222.5	12.7	335	1 TWK8_CAEEL	P34410 caenorhabd
2	178	10.2	691	1 TOK1_YEAST	P0310 saccharomyc
3	138	7.9	228	1 YMS1_CAEEL	Q10937 caenorhabd
4	121	6.9	333	1 Y13B_MERJA	Q57604 methanococc
5	116	6.6	417	1 KCH_ECOLI	P31069 escherichia
6	105	6.0	209	1 Y139_MERJA	Q37603 methanococc
7	100.5	5.7	391	1 NUPC_BACSU	P39141 bacillus su
8	97.5	5.6	356	1 YUXJ_BACSU	P0760 bacillus su
9	97	5.5	802	1 CIKB_RAT	P50052 rattus norv
10	95.5	5.4	363	1 AG22_HUMAN	P50052 homo sapien
11	95	5.4	853	1 CIKA_RAT	P15387 rattus norv
12	95	5.4	854	1 CIKA_HUMAN	Q14721 homo sapien
13	94.5	5.4	363	1 AG22_MOUSE	P35374 mus musculu
14	94.5	5.4	363	1 AG22_RAT	P35351 rattus norv
15	94	5.4	695	1 CIQ4_HUMAN	P56696 homo sapien
16	94	5.4	806	1 CIKB_HUMAN	Q92953 homo sapien
17	93.5	5.3	1174	1 CIEB_BACTA	Q03745 bacillus th
18	93	5.3	718	1 STJ3_YEAST	P39007 saccharomyc
19	92.5	5.3	363	1 AG22_MERUN	Q9206 meriones un
20	92	5.2	343	1 YD57_MERJA	Q58752 methanococc
21	91.5	5.2	663	1 CYOB_ECOLI	P18401 escherichia
22	91.5	5.2	674	1 TM1L_ARATH	P33543 arabidopsis
23	91.5	5.2	1159	1 HERG_HUMAN	Q12809 homo sapien
24	91.5	5.2	1174	1 CIKE_DROME	Q02280 drosophila
25	90.5	5.2	546	1 MUP3_YEAST	P38754 saccharomyc
26	90.5	5.2	580	1 P69_MYCAR	P15362 mycoplasma
27	90.5	5.2	2009	1 CIN1_RAT	P04774 rattus norv
28	90	5.1	899	1 YA8D_SCHPO	Q09778 schistosach
29	89.5	5.1	421	1 CDS1_ARATH	Q04928 a phosphati
30	89.5	5.1	872	1 CIQ3_HUMAN	Q43525 homo sapien
31	89.5	5.1	2223	1 CCAE_DISOM	P56699 discoppye o
32	89	5.1	350	1 FLHB_AQUAE	Q67813 aquifex aeo
33	89	5.1	388	1 YUBA_BACSU	Q32086 bacillus su

34	89	5.1	425	1 LIVM_ECOLI	P22729 escherichia
35	89	5.1	614	1 YDNK_LACTIC	P42377 lactococcus
36	88.5	5.0	484	1 ALTP_ECOLI	P75712 escherichia
37	88	5.0	425	1 LIVM_SALTY	P30236 salmonella
38	88	5.0	466	1 GABP_ECOLI	P25527 escherichia
39	87.5	5.0	415	1 GSCB_ECOLI	P30000 escherichia
40	87.5	5.0	470	1 CYCA_ECOLI	P39312 escherichia
41	87.5	5.0	518	1 GITL_YEAST	P25346 saccharomyc
42	87.5	5.0	624	1 PP51_HUMAN	Q43252 h bifunctio
43	87.5	5.0	924	1 CIKB_DROME	P17970 drosophila
44	87	5.0	672	1 CYOB_PSEPU	Q9WR2 pseudomonas
45	86.5	4.9	459	1 Y226_MYCGE	P47468 mycoplasma

ALIGNMENTS

RESULT	ID	TWK8_CAEEL	STANDARD	PRT	335 AA.
AC	P34410	TWK8_CAEEL			
DT	01-FEB-1994	(Rel. 28, Created)			
DT	01-FEB-1994	(Rel. 28, Last sequence update)			
DT	15-JUL-1998	(Rel. 36, Last annotation update)			
DE	TWK-8 PROTEIN.				
GN	TWK-8 OR F22B7.7.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;				
OC	Rhabdilitidae; Pelodierinae; Caenorhabditis.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPRAIN-BRISTOL NZ;				
RX	MEDLINE-94150718; PubMed-7906398;				
RA	Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,				
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,				
RA	Crexton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,				
RA	Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,				
RA	Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,				
RA	Larrelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,				
RA	Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showken R.,				
RA	Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,				
RA	Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,				
RA	Waterson R., Watson A., Weinstock L., Wilkinson-Sproot J.,				
RA	Woldman P.				
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.				
RT	elegans."				
RL	Nature 368:32-38(1994).				
CC	-1- SIMILARITY: TO POTASSIUM CHANNEL PROTEIN HAK-6.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; L12018; AA65460.1; -				
DR	WORMPEP; F22B7.7; CE00160.				
SO	SEQUENCE 335 AA; 38472 MW; 27DE7F1E79B3CA29 CRC64;				
Query Match 12.7%; Score 222.5; DB 1; Length 335;					
Best Local Similarity 27.0%; Pred. No. 5.3e-10;					
Matches 62; Conservative 50; Mismatches 63; Indels 55; Gaps 9;					
QY	92	VLNSAGNMWDPFSALEFASTVSTGTGHTVPSDGRACFIYSYIGIPFTLFLTA 151			
DB	19	VKNKATE-TWTFSSSIFFAVTVTITIGFNPVTNIGRWICLIFSLGIPLTLVTTAD 77			
QY	152	VVORTVHTVTRRPVLYFIRM-----GF-----SKQVVA-IV 182			
DB	78	LGFLESHLVWLYGNYLTKLTLILSRHKRREHVCHEHSHGMDNIEKRIPATLV 137			

QY 183 HAVILGCVTVSCFFPIPAVSVLEDDWVNFLESEFECFISLTIGLDYVPGEGYNQKR 242
 Db 138 LALLIVYTARG-----GVLMKSLK-PWSEFTSWFSLMTITVGGDLMPR-----R 183
 QY 243 ELKICGTCVLLGLIAML-----VLETFC-ELHEUKERKMFY 281
 Db 184 DGMVITLLIILIGKFSMKKOKKFLGLIATTCIDLVGVQYIKIRHY 233
 RESULT 2
 TOKI_YEAST
 ID TOKI_YEAST STANDARD: PRT: 691 AA.
 AC P40310: 005721:
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE OUTWARD-RECTIFIER POTASSIUM CHANNEL TOKI (TWO-DOMAIN OUTWARD RECTIFIER
 K+ CHANNEL YORK).
 GN TOKI OR DUK1 OR YIL093C OR J0911.
 OS Saccharomyces cerevisiae (Baker's yeast).
 Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 Saccharomycetaceae; Saccharomyces.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE-95076716; PubMed-7985424;
 RA Miosga T., Witzel A., Zimmermann F.K.;
 RT "Sequence and function analysis of a 9.46 kb fragment of
 RL Saccharomyces cerevisiae chromosome X.";
 RN Yeast 10:965-973(1994).
 [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN-NY13;
 RX MEDLINE-95379951; PubMed-7651518;
 RA Ketchum K.A., Joiner W.J., Sellers A.J., Kaczmarek L.K.,
 RL Goldstein S.A.N.;
 RT "A new family of outwardly rectifying potassium channel proteins with
 RL two pore domains in tandem.";
 RN Nature 376:690-695(1995).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96303826; PubMed-8723646;
 RA Reid J.D., Lukas W., Shafatian R., Bertl A., Scheurmann-Kettner C.,
 RL Guy H.R., North R.A.;
 RT "The S. cerevisiae outwardly-rectifying potassium channel (DUK1)
 RL identifies a new family of channels with duplicated pore domains.";
 RN Recept. Channels 4:51-62(1996).
 [4]
 RP SEQUENCE FROM N.A.
 RC Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M.,
 RL Romey G., Barhanin J.;
 RT Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: OUTWARDLY RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: SEEM TO BE COMPOSED OF TWO PORES.
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 CC -----
 DR EMBL; X77087; CA54360.1; -
 DR EMBL; Z49368; CA869386.1; -
 DR EMBL; U28005; AA49070.1; -
 DR EMBL; X94403; CA64176.1; -
 DR EMBL; U37254; AA49168.1; -
 DR PIR; S46585; S46585;
 DR PIR; S47058; S47058;
 DR SGD; S0003629; TOKI.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel.
 FT TRANSMEM 72 92
 FT TRANSMEM 138 158
 FT TRANSMEM 171 191
 FT TRANSMEM 204 224
 FT TRANSMEM 247 266
 FT TRANSMEM 302 322
 FT TRANSMEM 380 400
 FT TRANSMEM 436 456
 FT TRANSMEM 442 442
 FT TRANSMEM 512 512
 FT TRANSMEM 691 AA; 77407 MW; 507167E487B7AAAF CRC64;
 SO SEQUENCE
 Query Match 10.2%; Score 178; DB 1; Length 691;
 Best Local Similarity 25.4%; Pred. No. 2,7e-06;
 Matches 51; Conservative 33; Mismatches 71; Indels 46; Gaps 6;
 QY 97 SGMMNDFATLFPASTVSTGYGHTVPLSDGKACFIIVYIGIPFLPLFAVORI 156
 Db 267 SGLHITVYGNALFYCVSLITVGLDILPKSVGAKIMVLIFSLGSV--VLMGLIYFMTNR 324
 QY 157 TVHTRRPVLYFH-IRMGFSKO-----VVAI 181
 Db 325 IICKSSGPIFFEHVRVKGSKSKHMOSSKNLSEREAFDLKCIROTASRKOHWSLSV 384
 QY 182 HAVILGCVTVSCFFPIPAVSVLEDDWVNFLESEFECFISLTIGLDYVPGEGYNQKR 241
 Db 385 TIAIFM-----AFWILGALVFKEAE-MWSYFNCIFYFCLITIGYDYAPRIGAGNAF 437
 QY 242 RELYKIGTCVLLGLIAMLV 262
 Db 438 FVIMALG-AVPLMKALLSTV 456
 RESULT 3
 YMS1_CAEEL
 ID YMS1_CAEEL STANDARD: PRT: 228 AA.
 AC O10937:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHEICAL 25.6 KDA PROTEIN B0310.1 IN CHROMOSOME X.
 GN B0310.1.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RL Favello T.;
 RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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 CC -----
 DR EMBL; U40959; AAA81765.1; -
 DR MORPEP; B0310.1; CE03874.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 107 127
 FT TRANSMEM 138 158
 FT TRANSMEM 188 208
 FT TRANSMEM 228 AA; 25625 MW; 0822E836B3CA2360 CRC64;
 SO SEQUENCE
 Query Match 7.9%; Score 138; DB 1; Length 228;
 Best Local Similarity 23.7%; Pred. No. 0.00085;

Matches 50; Conservative 45; Mismatches 68; Indels 48; Gaps 10;

QY 70 LSEQLLEPLGRLVLEASNYGVSLSNAGNNMDFTSLFRASTYLSTGCHTYPLSDG 129
 DB 52 LADOLELTERALQ--HYGIDLKDS-----DKSPASGLQKSFATSTTIGPLVDDEFTTL 104
 QY 130 GKAECIIYSGVIGIPPTLLEFLAVVQRTIVVTRPVLVFLHFKSGSKOVAVIAHVALLGF 189
 DB 105 GKLIYVIALGTP---LFLVIGQ-----LGNVTSVWGCTTLM 142
 QY 190 VTSCEFPFIPAVSVLE---DWMNFLESFECFISLSTIGADYVPEGYNQKRELYK 246
 DB 143 VTI-VYIFISAVYDIVGSDVDYFIAIFSIQLQFTTGEVD-----NEFHG 190
 QY 247 IGITCYLLGLIAMLVLETFCCL-HELKKE 276
 DB 191 VLPYCIIVLGL-ALITAL--YQEMOHNIERF 218

RESULT 4
 ID Y13B_METUA STANDARD; PRT: 333 AA.
 AC Q57604;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PUTATIVE POTASSIUM CHANNEL PROTEIN M00138.1.
 GN M00138.1.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 NC Methanococcus.
 RC [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerecavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fullman J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sacow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.F., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: STRONG. TO M. JANNASCHII M01357.
 CC -1- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNELS.
 CC -----
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 CC -----
 DR EMBL: U67471; AAB98130.1; -;
 DR TIGR: M0138.1; -;
 KM Hypothetical protein; Transmembrane; Transport; Ion transport;
 FT Ionic channel. 7
 FT TRANSMEM 30 50 POTENTIAL.
 FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 81 POTENTIAL.
 SO SEQUENCE 333 AA; 37149 MW; 7CC082675F96B06A CRC64;

Query Match 6.9%; Score 121; DB 1; Length 333;
 Best Local Similarity 26.4%; Pred. No. 0.025;
 Matches 38; Conservative 25; Mismatches 63; Indels 18; Gaps 6;
 QY 187 LGFVTSCEFPFIPAVSVLEDDNMFLESFECFISLSTIGLGDYVPEGYNQKRELYK 246

DB 9 LGITVYIIIIIIILESVIIMTVE-GMDFTAFTAVTISTVGGDTP-----QTF--LGR 60
 QY 247 IGITCYLLGLIAMLVLETFCCLHELKFRKMFYKKDKDE---DQVHIEHDLSFS 302
 DB 61 LSVIITIFAGVAVAYVTGNIAISFEIEGHFRKRYFLRKMORIKLNHYYI-----CGYG 116
 QY 303 SITDPAAGKREKQKNEPEFVATQS 326
 DB 117 RLGVYIA--EERKCNIPFVIIDS 138

RESULT 5
 ID KCH_ECOLI STANDARD; PRT: 417 AA.
 AC P31069; P94716; P94717; P94723; P94729; P97198; P97225;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PUTATIVE POTASSIUM CHANNEL PROTEIN.
 GN KCH.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 NC Escherichia.
 RC [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / W3110;
 RX MEDLINE=94224769; PubMed=8170937;
 RA Milkman R.;
 RA "An Escherichia coli homologue of eukaryotic potassium channel
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3510-3514(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12, AND VARIOUS ECOR STRAINS;
 RA Milkman R.;
 RN Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / M31655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RL "The complete genome sequence of Escherichia coli K-12.";
 RN Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Alpha H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubram S.,
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horiuchi T.;
 RL "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE DEFENSE AGAINST OSMOTIC SHOCK.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (POTENTIAL).
 CC -1- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNELS.
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 CC -----

CC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE-96134975; PubMed-8550462;
RA Saxild H.H., Andersen L.N., Hammer K.;
RT "dra-nupc-pdp operon of Bacillus subtilis: nucleotide sequence,
RL induction by deoxyribonucleosides, and transcriptional regulation by
J. Bacteriol. 178:424-434(1996).
[2]
SEQUENCE FROM N.A.
RC STRAIN-168 / BGSC1A1;
RX MEDLINE-97021444; PubMed-8867804;
RA Yoshida K.-I., Fujitama M., Yanai N., Fujita Y.;
RT "Cloning and sequencing of a 23-bp region of the Bacillus subtilis
genome between the *lcl* and *hut* operons.";
DNA Res. 2:295-301(1995).
[3]
SEQUENCE FROM N.A.
RC STRAIN-168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
SUBMITTED (NOV-1997) TO THE EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE SLC28A FAMILY OF TRANSPORTERS.

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DR EMBL: X82174; CAAS7663.1; -
DR EMBL: D45912; BAA08338.1; -
DR EMBL: Z99124; CAB15977.1; -
DR SUBMITTER: BG10984; NUPEC.
DR INTERPRO: IPR02668; -
DR PFAM: PF01773; Nucleoside_ttra2; 1.
DR Transport; Transmembrane.
FT TRANSMEM 3 23 POTENTIAL.
FT TRANSMEM 32 52 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 168 188 POTENTIAL.
FT TRANSMEM 191 211 POTENTIAL.
FT TRANSMEM 249 269 POTENTIAL.
FT TRANSMEM 272 292 POTENTIAL.
FT TRANSMEM 335 355 POTENTIAL.
FT TRANSMEM 372 392 POTENTIAL.
FT CONFLICT 16 16 F->L (IN REF. 2).
FT CONFLICT 304 305 SI->RL (IN REF. 1).
FT CONFLICT 320 320 S->V (IN REF. 1).
SQ SEQUENCE 393 AA; 42529 MW; C28677B5D30AE0AC CRC64;

Query Match 5.7%; Score 100.5; DB 1; Length 393;
Best Local Similarity 25.0%; Pred. No. 1;
Matches 56; Conservative 32; Mismatches 89; Indels 47; Gaps 10.

DY 194 CFFFLPAVFEVSLEDDNMFLESF-----YFCFISLTSLGL 228

	DB	348	SIGITAGAVKGLNKGQNVVAFGKLXLYGATLVSFLSAIVGL	391	: :
	RESULT	8			: : :
	YUXJ_BACSU				
ID	YUXJ_BACSU	STANDARD:	PRT:	356 AA.	
AC	P40760:				
DT	01-FEB-1995 (Rel. 31, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	HYPOTHETICAL 39.1 KDA PROTEIN IN KAPD-PBPD INTERGENIC REGION (ORF1).				
GN	YUXJ				
OS	Bacillus subtilis.				
OC	Bacteria; Firmicutes; Bacillus/clostridium group;				
OC	Bacillus/Staphylococcus group; Bacillus.				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RP	STRAIN-168;				
RX	MEDLINE=97419515; PubMed=9274030;				
RA	Oudega B., Koningssteijn G., Rodrigues L., de Sales Ramon M.,				
RA	Hilbert H., Duesterhoeft A., Pohl T.M., Weltzenegger T.;				
RT	"Analysis of the Bacillus subtilis genome: cloning and nucleotide				
RT	sequence of a 62 kb region between 275 degrees (rnb) and 284 degrees				
RT	(pat).";				
RL	Microbiology 143:2769-2774(1997).				
RN	[2]				
RP	SEQUENCE OF 101-356 FROM N.A.				
RC	STRAIN-168;				
RX	MEDLINE=95050302; PubMed=7961491;				
RA	Popham D.L., Setlow P.;				
RT	"Cloning, nucleotide sequence, mutagenesis, and mapping of the				
RT	Bacillus subtilis pbpd gene, which codes for penicillin-binding				
RT	protein 4.";				
RL	J. Bacteriol. 176:7197-7205(1994).				
CC	-I SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)				
CC	-I SIMILARITY: STRONG, TO E.COLI YCBE. SOME, TO THE DRUG RESISTANCE				
CC	TRANSLOCASE FAMILY.				
CC					
CC	-----				
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL: Z93933; CAB07914.1; -				
DR	EMBL: Z99120; CAB15137.1; -				
DR	EMBL: U11882; AAA64942.1; -				
DR	SUBTILLIST; BG10976; YUXJ.				
KW	Hypothetical protein; Transmembrane.				
FT	TRANSMEM 39 59 POTENTIAL.				
FT	TRANSMEM 61 81 POTENTIAL.				
FT	TRANSMEM 92 112 POTENTIAL.				
FT	TRANSMEM 119 139 POTENTIAL.				
FT	TRANSMEM 159 179 POTENTIAL.				
FT	TRANSMEM 201 221 POTENTIAL.				
FT	TRANSMEM 236 256 POTENTIAL.				
FT	SEQUENCE 356 AA; 39105 MW; 31758C0122231311 CRC64;				
Query Match	5.6%; Score 97.5; DB 1; Length 356;				
Best Local Similarity	22.0%; Pred. No. 1.6;				
Matches	72; Conservative 34; Mismatches 119; Indels 103; Gaps 12,				
0Y	3 QSLASSCVRLVERHRSAMCFGLVLGYL-----LYLVGAVFSSVELPYEDLLRQ 54	:	:	:	:
Dd	83 KSSAQKTGIQTLOMGGVSGLSIFGLPLGMADRFQTFYYFFITSFYFSVVLLVLFGVKRK 142	:	:	:	:
0Y	55 EL--KKLRRLFLEHECLIS-----EQQLDFQLGTVLASNGVSVLASASGNMMMDIFS 106	:	:	:	:
Dd	143 HALETARTSYSRREVSIYFHHPDALWMMLTLIQGNSIOPLALVYNELHGPNV 202	:	:	:	:


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RC TISSUE-BLOOD; PubMed=7945336;
RX MEDLINE=95032069; PubMed=7945336;
RA Koike G., Horiuchi M., Yamada T., Sepirer C., Jacob H.J., Dzau V.J.;
RT "Human type 2 angiotensin II receptor gene: cloned, mapped to the X
RL chromosome, and its mRNA is expressed in the human lung.";
RN Biochem. Biophys. Res. Commun.. 203:1842-1850(1994).
RP [4]
RC SEQUENCE FROM N.A.
RX MEDLINE=94242007; PubMed=8185599;
RA Tsuzuki S., Ichiki T., Nakakubo H., Kitami Y., Iino D.F.,
RT Shira H., Itagami T.;
RL "Molecular cloning and expression of the gene encoding human
RN angiotensin II type 2 receptor.";
RP Biochem. Biophys. Res. Commun.. 200:1449-1454(1994).
RX [5]
RC SEQUENCE FROM N.A.
RX TISSUE-LUNG;
RA MEDLINE=95091796; PubMed=7999093;
RT Martin M.M., Su B., Elton T.S.;
RL "Molecular cloning of the human angiotensin II type 2 receptor cDNA.";
RN Biochem. Biophys. Res. Commun.. 205:645-651(1994).
RX [6]
RC SEQUENCE FROM N.A.
RX TISSUE-PLACENTA;
RA MEDLINE=95236034; PubMed=7719706;
RT Laarad D., Blend-Sutren M.M., Villagoeis P., Mattel M.-G.,
RN Strohsberg A.D., Nahmias C.;
RL "Molecular characterization and chromosome localization of a human
RN angiotensin II AT2 receptor gene highly expressed in fetal tissues.";
RX Recept. Channels 2:271-280(1994).
RN [7]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE-BLOOD;
RA Katsuya T., Dzau V.J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 1-16 FROM N.A.
RC TISSUE-UTERUS;
RA Warnecke C.H., Holzmelster J., Regitz-Zagrosek V., Fleck E.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MAY HAVE A ROLE IN CELL
CC PHORPHOGENESIS AND RELATED EVENTS IN GROWTH AND DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: IN ADULT, HIGHLY EXPRESSED IN MYOMETRIUM WITH
CC LOWER LEVELS IN ADRENAL GLAND AND FALLOPIAN TUBE. VERY HIGHLY
CC EXPRESSED IN FETAL KIDNEY AND INTESTINE.
CC -1- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb.ch).
CC -----
CC EMBL: U20860; AAA85851.1; -
CC EMBL: L34579; AAA98990.1; -
CC EMBL: U10273; AAA61794.1; -
CC EMBL: U15592; AAA50762.1; -
CC EMBL: U16957; AAA67753.1; -
CC EMBL: U27478; AAA84900.1; -
CC EMBL: X87723; CAA61022.1; -
CC HSSP: P34996; IDDD.
CC
CC GCRDB: GCR_1057; -
CC GCRDB: GCR_1245; -
CC GCRDB: GCR_1876; -
CC GCRDB: GCR_2011; -
CC GCRDB: GCR_2027; -
CC GCRDB: GCR_2031; -
CC GCRDB: GCR_2056; -
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CC MIM: 300034; -.

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DR	INTERPRO: IPR000147; -	
DR	INTERPRO: IPR000248; -	
DR	INTERPRO: IPR000276; -	
DR	PFAM: PF00001; 7tm_1; 1.	
DR	PRINTS: PR00237; GPCRHDOPSN.	
DR	PRINTS: PR00241; ANGIOTENSINR.	
DR	PRINTS: PR00636; ANGIOTENSIN2R.	
DR	PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; 1.	
DR	PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.	
FT	DOMAIN	1 45
FT	TRANSMEM	46 71
FT	DOMAIN	72 80
FT	TRANSMEM	81 102
FT	DOMAIN	103 119
FT	TRANSMEM	120 140
FT	DOMAIN	141 160
FT	TRANSMEM	161 179
FT	DOMAIN	180 208
FT	TRANSMEM	209 234
FT	DOMAIN	235 256
FT	TRANSMEM	257 278
FT	DOMAIN	279 285
FT	TRANSMEM	286 313
FT	DOMAIN	314 363
FT	CARBOHYD	4 4
FT	CARBOHYD	13 13
FT	CARBOHYD	24 24
FT	CARBOHYD	29 29
FT	CARBOHYD	34 34
FT	CONFLICT	268 269
FT	CONFLICT	272 272
FT	CONFLICT	323 323
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	Query Match	5.4%; Score 95.5; DB 1; Length 363;
	Best Local Similarity	20.9%; Pred. No. 2.3;
	Matches	60; Conservative 40; Mismatches 80; Indels 107; Gaps 16;
OY	17 HRSACFGEFL--VGYLLYL-VEGAVVF---SSVELPEYEDLLROELKRLKEEHL--67	
	: : : : : : : : : : : : : : : :	
Db	106 YRDMLEFGPVACKVGSFLTLMFPASIFFTICMSVD-RQSVITYFFLSQRHPMQASTIV164	
OY	68 -----ECLSPQOLEQFLGRVLEASN-----GVSLSNAGMNN101	
	: : : : : : : : : : : : : : : :	
Db	165 PLVMCMACLS--SLEPTFEFDVRTIEYLGNVNCIAPPEKYAQMAGALMKNLIG---219	
OY	102 WDFTSALFFAST-----VLSTTGCGHYPLSG--GKAFITLISVGIRP-TLTF148	
	: : : : : : : : : : : : : : : :	
Db	220 --FILPLFIETCYEGIRKHHLKTNSYGKNRIITRQVLKMAAAVVLAFLICMLPHVILTF277	
OY	149 LTAAVQRTIVHTRRPVLYEHIRMGFSAOVAIV----HAVLGFMVSCEFLPAAVE203	
	: : : : : : : : : : : : : : : :	
Db	278 LDALAMMGVIN-----SCEVIAVIDLALPFLTLGF-TNSC-----312	
OY	204 SVLEDMMNLFSEFYECFISTLTIGLDVDPGEGYNOKRELIKIGIT250	
	: : : : : : : : : : : : : : : :	
Db	313 -----VNPFIXCFV-----GNRFQOKLRISVERPIIT338	
 RESULT 11		
C1KA_RAT	C1KA_RAT	PRT; 853 AA.
AC	P15387;	
DT	01-APR-1990 (Rel. 14, Created)	
DT	01-AUG-1990 (Rel. 15, Last sequence update)	
DT	15-DEC-1998 (Rel. 37, Last annotation update)	
DE	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).	
GN	KCNB1.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	

```

[1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN:
RX MEDLINE=89365157; PubMed=2770868;
RA Frech G.C., Vandongen A.M.J., Schuster G., Brown A.M., Joho R.H.;
RT "A novel potassium channel with delayed rectifier properties isolated
RL from rat brain by expression cloning.";
RN Nature 340:642-645(1989).
RP
RP REVISIONS.
RA Frech G.C.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
CC
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC
CC -I- TISSUE SPECIFICITY: IN THE BRAIN, THE GREATEST DENSITY OCCURS IN
CC THE CEREBRAL CORTEX, FOLLOWED BY THE HIPPOCAMPUS, CEREBELLUM, AND
CC OLFACTORY BULB. IN PERIPHERAL TISSUES IT IS MOST PROMINENT IN
CC RETINA AND KIDNEY. ALSO PRESENT IN CARDIAC MUSCLE TISSUE OF THE
CC ARRIUM AND VENTRICLE AND IN SKELETAL MUSCLE.
CC
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC
CC -I- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC
CC
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CC -----
DR EMBL; X16476; CAA34497.1; -.
DR PIR; S05448; CHRTD1.
DR INTERPRO; IPR000636; -.
DR INTERPRO; IPR003091; -.
DR Pfam; PF00520; Ion.trans; 1.
DR PRINTS; PR00169; KCANNEL.
KW Ion channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT DOMAIN 1 182
FT TRANSMEM 183 204
FT DOMAIN 205 224
FT TRANSMEM 225 246
FT DOMAIN 247 256
FT TRANSMEM 257 278
FT DOMAIN 279 290
FT TRANSMEM 291 312
FT DOMAIN 313 326
FT TRANSMEM 327 348
FT DOMAIN 349 388
FT TRANSMEM 389 410
FT DOMAIN 411 853
FT CARBOHYD 279 279
FT MOD_RES 440 440
FT MOD_RES 492 492
FT MOD_RES 492 492
FT SEQUENCE 853 AA; 95280 MW; 7A08998839716165 CRC64;

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OY	13	IIVERRRASACFGFVLVGLIVLPGAVNVSSVELPEDELRLKTKRPRLEHHCCLSE	72
Dd	174	LLEKRNSVAAKIILAIISIMFIVLSIALSLMTLP-----ELQSLD----EFGOSTN	222
OY	73	QQLEQFLGRVLEA-----SNYGVSVLMSAGNMWDETSALFFASTVLSITTYGHTVP	125
Dd	223	POLAH-----VEAVCIAMFTMEYLDFLRFSPPK---KKRFKPKPLNADILLALPYVTIF	274
OY	126	LSDGKA---PCLITSVICIPPTLLFLPAVVOIRIVHYTRRVLYPHIMWGSKOVAALV	182
Dd	275	LTESKSVLVQFNVRVVQI-PRIKRIKLIL-KLARHSIGLOSGTTLRSNYEL-----	327
OY	183	HAVILGFVTVSCFEFPPIPAVFSL-EDWNMFEE-----SFFCFISTSLTGIDGVPCEGYN	238
Dd	328	-GLLIIFLAMGMITSISSLVEFAEKREDDTKFSISAFSEFMATITMYTGGDIYRK----	382
OY	239	QKRELKYNI-GITCY--LLGLIAMLVLETFCETHELK 275	
Dd	383	---TLKGIVGGLCCIAGLVIALPIPIVNNESEFYRKQK 420	
 RESULT 12 CIRKA_HUMAN STANDARD; PRG: 854 AA.			
ID AC	CIRKA_HUMAN	STANDARD;	PRG: 854 AA.
DT DT	15-JUL-1998 (Rel. 36, Created)		
DT DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT DT	15-JUL-1998 (Rel. 36, Last annotation update)		
DE DE	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DHK1).		
GN GN	KCNB1.		
OS OS	Homo sapiens (Human).		
OC OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
RN RN	[1]		
RP RP	SEQUENCE FROM N.A.		
RA RA	Ikedo S.R., Soler F., Zuhlke R.D., Joho R.H., Lewis D.L.;		
RL RL	Submitted (JAN-1993) to the EMBL/Genbank/DBJ databases.		
CC CC	-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM		
CC CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED		
CC CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE		
CC CC	MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH		
CC CC	WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL		
CC CC	GRADIENT.		
CC CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC CC	-1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS		
CC CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT		
CC CC	EVERY THIRD POSITION.		
CC CC	-1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL		
CC CC	ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR		
CC CC	COMPARTMENTS.		
CC CC	-1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER		
CC CC	CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.		
CC CC	-----		
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CC CC	-----		
DR DR	EMBL; L02840; AAA36156.1; -		
DR DR	MIM; 600397; -		
DR DR	INTERPRO; IPRO00636; -		
DR DR	INTERPRO; IPRO03091; -		
DR DR	PFAM; PF00520; Ion_trans_1.		
DR DR	PRINTS; PR00169; KCCHANNEL.		
KW KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;		
KW KW	Glycoprotein; Multigene family; Phosphorylation.		
FT FT	DOMAIN 1 182 CYTOPLASMIC (POTENTIAL).		
FT FT	TRANSHEM 183 204 SEGMENT S1 (POTENTIAL).		
FT FT	DOMAIN 205 224 EXTRACELLULAR (POTENTIAL).		

FT TRANSMEM 225 246 SEGMENT S2 (POTENTIAL).
 FT DOMAIN 247 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 278 SEGMENT S3 (POTENTIAL).
 FT DOMAIN 279 290 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 291 312 SEGMENT S4 (POTENTIAL).
 FT DOMAIN 313 326 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 327 348 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 349 388 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 389 410 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 411 854 CYTOPLASMIC (POTENTIAL).
 FT MOD.RES 440 440 PHOSPHORYLATION (HY CAPK)
 FT MOD.RES 440 440 (POTENTIAL).
 FT MOD.RES 492 492 PHOSPHORYLATION (HY CAPK)
 FT MOD.RES 492 492 (POTENTIAL).
 FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 854 AA: 95521 MW: 360DEB3E45731EDA CRC64;

Query Match 5.4%; Score 95; DB 1; Length 854;
 Best Local Similarity 21.7%; Pred. No. 6.3;
 Matches 61; Conservative 55; Mismatches 113; Indels 52; Gaps 14;

QY 13 LVERHSAMCGFLVGLVLYVFGAVSSVELPYEDLLRDLRLKRLRLEEHECLSE 72
 DB 174 LLEKPNSSVAKKILAIISIMFIVLSTIALSLNTLP-----ELQSLD---EFGQSTDN 222
 QY 73 QOLEQFLGRVLEA-----SNYGVSVLSNASGNMMMDTSALFFASTVSTGYGHTVP 125
 DB 223 POLAH-----VEAVCIAMFTMEILNPLSPK---KMKPEKGPLMALDLAILPYVTIF 274
 QY 126 LSDGKA---FCIIYVIGIPFLFLFAVQRITVTRPVLVFIHMGFSKOVAIV 182
 DB 275 LTSNSNVLOFQVNRVVOQ-FRIMRLRL-KLARHSTLOSLGFLRNSYML----- 327
 QY 183 HAVLGFVTVSCFFIIPAAVESVL-EDDNMFLE---SEYFCFISLSTIGLDVYPGEGYN 238
 DB 328 -GLIIFLAMGIMFSSILVFAEKDEDTFKSKIPASFWATITMTVGYGDIYPRK---- 382
 QY 239 QKRELYKI--GITCY--LLGLIAMIVLETCELHELKK 275
 DB 383 ---TLGKIVGGLCGIAGLVIALPIPIVNNSEFYKEOK 420

RESULT 13
 AG22_MOUSE STANDARD: PRT: 363 AA.
 ID AG22_MOUSE P35374;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE TYPE-2 ANGIOTENSIN II RECEPTOR (AT2).
 GN AGTR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-FETAL.
 RX MEDLINE-94092107; PubMed-8267573;
 RA Nakajima M., Mukoyama M., Pratt R.E., Horiuchi M., Dzau V.J.;
 RT "Cloning of cDNA and analysis of the gene for mouse angiotensin II
 RT type 2 receptor.";
 RL Biochem. Biophys. Res. Commun. 197;393-399(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE-9412216; PubMed-8292631;
 RA Ichiki T., Herold C.L., Kamabayashi Y., Bardhen S., Inagami T.;
 RT "Cloning of the cDNA and the genomic DNA of the mouse angiotensin II
 RT type 2 receptor.";
 RL Biochim. Biophys. Acta 1189;247-250(1994).
 RN [3]
 RP SEQUENCE FROM N.A.

RX MEDLINE-96337434; PubMed-8726696;
 RA Nallamas C., Cazaubon S.M., Sutren M., Masson M., Lazard D.,
 RA Villagras P., Elbaz N., Strosberg A.D.;
 RT "Molecular and functional characterization of angiotensin II AT2
 RT receptor in neuroblastoma NIE-115 cells.";
 RL Adv. Exp. Med. Biol. 396:167-173(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-LIVER;
 RX MEDLINE-95378283; PubMed-7650042;
 RA Horiuchi M., Koike G., Yamada T., Nakajima M.,
 RA Dzau V.J.;
 RT "The growth-dependent expression of angiotensin II type 2 receptor is
 RT regulated by transcription factors interferon regulatory factor-1 and
 RT -2.";
 RL J. Biol. Chem. 270:20225-20230(1995).
 CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MAY HAVE A ROLE IN CELL
 CC MORPHOGENESIS AND RELATED EVENTS IN GROWTH AND DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN FETUS, LOWER LEVELS IN ADULT
 CC BRAIN.
 CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: S67465; AAB29336.1; -
 CC EMBL: U04828; AAC52128.1; -
 CC EMBL: U00766; AAC04933.1; -
 CC EMBL: L32840; AAB49539.1; ALT_INIT.
 CC EMBL: U11073; AAB48184.1; -
 CC PIR: JC2028; JC2028.
 CC HSSP: P34996; 1DD0.
 CC GCRDB: GCR_0890; -
 CC GCRDB: GCR_1007; -
 CC GCRDB: GCR_1010; -
 CC MGD: MGI:87966; AGTR2.
 CC INTERPRO: IPR000147; -
 CC INTERPRO: IPR000248; -
 CC INTERPRO: IPR000276; -
 CC PFM: PFM0001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCRHHODPSN.
 CC PRINTS: PR00241; ANGIOTENSINR.
 CC PRINTS: PR00636; ANGIOTENSINR.
 CC PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 CC PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; glycoprotein;
 CC Phosphorylation.
 CC
 CC FT DOMAIN 1 45
 CC FT TRANSMEM 46 71
 CC FT DOMAIN 72 80
 CC FT TRANSMEM 81 102
 CC FT DOMAIN 103 119
 CC FT TRANSMEM 120 140
 CC FT DOMAIN 141 160
 CC FT TRANSMEM 161 179
 CC FT DOMAIN 180 208
 CC FT TRANSMEM 209 234
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 CC FT TRANSMEM 257 278
 CC FT DOMAIN 279 285
 CC FT TRANSMEM 286 313
 CC FT DOMAIN 314 363
 CC FT CARBOHYD 4 4
 CC FT CARBOHYD 13 13
 CC FT CARBOHYD 24 24
 CC FT CARBOHYD 29 29
 CC
 CC 1 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 2 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 3 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 4 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 5 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 6 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 7 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).

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